SEQUENCE LISTING

<110> Dixon, Richard A.
     Xia, Yiji
     Lamb, Christopher

<120> CONSTITUTIVE DISEASE RESISITANCE (CDR1)
     GENE AND METHODS OF USE THEREOF

<130> SALK2820-1

<140> 09/353,332
<141> 1999-07-14

<150> 60/092,696
<151> 1998-07-14

<160> 3

<170> FastSEQ for Windows Version 4.0

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<213> Arabidopsis thaliana

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<222> (1111)...(2421)

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gcgataaagg aaaggctatc gttcaagatg cctctaccga cagtggtccc aaagatggac       240
ccccacccac gaggaacatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag       300
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aaatgagaaa atcttcactt ttatttattc ttaatacgtc agattctctg aacacaaaat       960
gatataattt gtagataact tactcaaaac gtaagaactc actatctatt atcatttatt      1020
aaccaccatc tcattaatct tataaatatg tactcattag attgtcaaaa gtaaaacctc      1080
acaatacact ttaaactaca aatcaaaaca atg gcc tct cta ttc tct tca gtt      1134
                                    Met Ala Ser Leu Phe Ser Ser Val
                                     1                   5

ctc ttg tct ctt tgt tta ctc tct tca ctt ttt ctc tca aat gca aac      1182
Leu Leu Ser Leu Cys Leu Leu Ser Ser Leu Phe Leu Ser Asn Ala Asn
     10                  15                  20

gct aag cca aaa cta ggc ttc acc gcg gat cta atc cac cgt gat tct      1230
```

```
                                                                    Ala Lys Pro Lys Leu Gly Phe Thr Ala Asp Leu Ile His Arg Asp Ser
                                                                    25              30              35              40
```

```
cct aaa tcg ccg ttc tat aac ccg atg gaa acc tct tcc cag cgt cta    1278
Pro Lys Ser Pro Phe Tyr Asn Pro Met Glu Thr Ser Ser Gln Arg Leu
                45              50              55
```

```
cga aac gcg atc cac cga tcc gtt aac cgt gtt ttc cat ttc act gaa    1326
Arg Asn Ala Ile His Arg Ser Val Asn Arg Val Phe His Phe Thr Glu
                60              65              70
```

```
aag gat aac aca cca caa cca cag att gac ctc acc tca aat agc ggt    1374
Lys Asp Asn Thr Pro Gln Pro Gln Ile Asp Leu Thr Ser Asn Ser Gly
                75              80              85
```

```
gaa tat ctc atg aac gta tcc att gga aca cct cct ttc ccg atc atg    1422
Glu Tyr Leu Met Asn Val Ser Ile Gly Thr Pro Pro Phe Pro Ile Met
                90              95              100
```

```
gcc atc gcc gac acc gga agt gat ctc ctc tgg acg cag tgc gca cca    1470
Ala Ile Ala Asp Thr Gly Ser Asp Leu Leu Trp Thr Gln Cys Ala Pro
105             110             115             120
```

```
tgc gat gat tgt tac act caa gtt gat cct ctc ttt gac cct aaa acg    1518
Cys Asp Asp Cys Tyr Thr Gln Val Asp Pro Leu Phe Asp Pro Lys Thr
                125             130             135
```

```
tct tcc aca tac aaa gac gtt tct tgc tcc tca agt caa tgt act gcc    1566
Ser Ser Thr Tyr Lys Asp Val Ser Cys Ser Ser Ser Gln Cys Thr Ala
                140             145             150
```

```
cta gaa aat caa gcc tct tgt tcc aca aat gac aac act tgt tct tac    1614
Leu Glu Asn Gln Ala Ser Cys Ser Thr Asn Asp Asn Thr Cys Ser Tyr
                155             160             165
```

```
tca ttg tct tac ggg gat aac tca tac aca aag ggt aac atc gcc gtg    1662
Ser Leu Ser Tyr Gly Asp Asn Ser Tyr Thr Lys Gly Asn Ile Ala Val
                170             175             180
```

```
gat acc tta acg ctc ggc tcc agc gat acc cgc cct atg cag ctt aag    1710
Asp Thr Leu Thr Leu Gly Ser Ser Asp Thr Arg Pro Met Gln Leu Lys
185             190             195             200
```

```
aat att att atc ggt tgt ggt cac aac aac gct gga acg ttt aac aag    1758
Asn Ile Ile Ile Gly Cys Gly His Asn Asn Ala Gly Thr Phe Asn Lys
                205             210             215
```

```
aaa ggc tct gga atc gtc gga cta ggt ggt ggt ccg gtt tcg ctt atc    1806
Lys Gly Ser Gly Ile Val Gly Leu Gly Gly Gly Pro Val Ser Leu Ile
                220             225             230
```

```
aag caa ctt ggc gac tcc atc gac ggt aaa ttc tca tac tgc ttg gtt    1854
Lys Gln Leu Gly Asp Ser Ile Asp Gly Lys Phe Ser Tyr Cys Leu Val
                235             240             245
```

```
cct cta act tcc aaa aag gat caa acg agt aaa atc aac ttc gga acc    1902
Pro Leu Thr Ser Lys Lys Asp Gln Thr Ser Lys Ile Asn Phe Gly Thr
250             255             260
```

```
aat gcc atc gtg tcg gga tca gga gtt gtc tca act cct ctg atc gca    1950
```

```
Asn Ala Ile Val Ser Gly Ser Gly Val Val Ser Thr Pro Leu Ile Ala
265             270             275             280
```

```
aag gcg tct caa gag acc ttc tat tac cta acc cta aaa tcc att agc    1998
Lys Ala Ser Gln Glu Thr Phe Tyr Tyr Leu Thr Leu Lys Ser Ile Ser
                285             290             295
```

```
gtg gga agc aag caa atc caa tac tca ggc tca gat tct gaa agc agc    2046
Val Gly Ser Lys Gln Ile Gln Tyr Ser Gly Ser Asp Ser Glu Ser Ser
                300             305             310
```

```
gag gga aac atc atc atc gat tca ggc aca act tta acg tta tta ccg    2094
Glu Gly Asn Ile Ile Ile Asp Ser Gly Thr Thr Leu Thr Leu Leu Pro
                315             320             325
```

```
act gaa ttt tac tcc gag ctc gag gat gcg gtt gca tcc tct atc gat    2142
Thr Glu Phe Tyr Ser Glu Leu Glu Asp Ala Val Ala Ser Ser Ile Asp
        330             335             340
```

```
gct gag aag aag caa gat cca caa agc ggt ttg agt cta tgt tac agt    2190
Ala Glu Lys Lys Gln Asp Pro Gln Ser Gly Leu Ser Leu Cys Tyr Ser
345             350             355             360
```

```
gca acc gga gat cta aaa gtt cca gtc att act atg cat ttt gat gga    2238
Ala Thr Gly Asp Leu Lys Val Pro Val Ile Thr Met His Phe Asp Gly
                365             370             375
```

```
gcc gat gtg aag ctt gac tcc tcc aat gcc ttt gta caa gtc tcg gag    2286
Ala Asp Val Lys Leu Asp Ser Ser Asn Ala Phe Val Gln Val Ser Glu
                380             385             390
```

```
gat ttg gtt tgc ttt gcc ttc cgc gga agc ccg agt ttc tcc ata tac    2334
Asp Leu Val Cys Phe Ala Phe Arg Gly Ser Pro Ser Phe Ser Ile Tyr
            395             400             405
```

```
ggt aat gtg gcg cag atg aac ttt ctt gtt gga tac gac act gtt tcc    2382
Gly Asn Val Ala Gln Met Asn Phe Leu Val Gly Tyr Asp Thr Val Ser
        410             415             420
```

```
aaa acg gtg tca ttt aag cca aca gat tgt gca aag atg tagttgtttc     2431
Lys Thr Val Ser Phe Lys Pro Thr Asp Cys Ala Lys Met
425             430             435
```

```
atctcaacat gtttttcaaa attgtgtttt caattacaat aatggctgat ttagtttcag   2491
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Ala Asp Leu Ile His Arg Asp Ser Pro Lys Ser Pro Phe Tyr Asn Pro
        35   40   45
Met Glu Thr Ser Ser Gln Arg Leu Arg Asn Ala Ile His Arg Ser Val
    50   55   60
Asn Arg Val Phe His Phe Thr Glu Lys Asp Asn Thr Pro Gln Pro Gln
65   70   75   80
Ile Asp Leu Thr Ser Asn Ser Gly Glu Tyr Leu Met Asn Val Ser Ile
                85   90   95
Gly Thr Pro Pro Phe Pro Ile Met Ala Ile Ala Asp Thr Gly Ser Asp
            100   105   110
Leu Leu Trp Thr Gln Cys Ala Pro Cys Asp Asp Cys Tyr Thr Gln Val
        115   120   125
Asp Pro Leu Phe Asp Pro Lys Thr Ser Ser Thr Tyr Lys Asp Val Ser
    130   135   140
Cys Ser Ser Ser Gln Cys Thr Ala Leu Glu Asn Gln Ala Ser Cys Ser
145   150   155   160
Thr Asn Asp Asn Thr Cys Ser Tyr Ser Leu Ser Tyr Gly Asp Asn Ser
                165   170   175
Tyr Thr Lys Gly Asn Ile Ala Val Asp Thr Leu Thr Leu Gly Ser Ser
            180   185   190
Asp Thr Arg Pro Met Gln Leu Lys Asn Ile Ile Ile Gly Cys Gly His
        195   200   205
Asn Asn Ala Gly Thr Phe Asn Lys Lys Gly Ser Gly Ile Val Gly Leu
    210   215   220
Gly Gly Gly Pro Val Ser Leu Ile Lys Gln Leu Gly Asp Ser Ile Asp

```
225                   230                   235                   240
Gly Lys Phe Ser Tyr Cys Leu Val Pro Leu Thr Ser Lys Lys Asp Gln
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Thr Ser Lys Ile Asn Phe Gly Thr Asn Ala Ile Val Ser Gly Ser Gly
              260                   265                   270
Val Val Ser Thr Pro Leu Ile Ala Lys Ala Ser Gln Glu Thr Phe Tyr
              275                   280                   285
Tyr Leu Thr Leu Lys Ser Ile Ser Val Gly Ser Lys Gln Ile Gln Tyr
          290                   295                   300
Ser Gly Ser Asp Ser Glu Ser Ser Glu Gly Asn Ile Ile Ile Asp Ser
305                   310                   315                   320
Gly Thr Thr Leu Thr Leu Leu Pro Thr Glu Phe Tyr Ser Glu Leu Glu
                  325                   330                   335
Asp Ala Val Ala Ser Ser Ile Asp Ala Glu Lys Lys Gln Asp Pro Gln
              340                   345                   350
Ser Gly Leu Ser Leu Cys Tyr Ser Ala Thr Gly Asp Leu Lys Val Pro
              355                   360                   365
Val Ile Thr Met His Phe Asp Gly Ala Asp Val Lys Leu Asp Ser Ser
          370                   375                   380
Asn Ala Phe Val Gln Val Ser Glu Asp Leu Val Cys Phe Ala Phe Arg
385                   390                   395                   400
Gly Ser Pro Ser Phe Ser Ile Tyr Gly Asn Val Ala Gln Met Asn Phe
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Asp Cys Ala Lys Met
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<213> Artificial Sequence

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<223> synthetic peptide utilized for antibody
      production; segment of SEQ ID NO:2

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